

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 29, 2002, 20:54:52 ; Search time 1417.73 Seconds

453.817 Million cell updates/sec

Title: US-09-432-546-15

Perfect score: 39

Sequence: 1 agggatggccttggtaatggcccttattt 39

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248389755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

No.	Score	Query	Match	Length	DB	ID	Description
c 1	24.6	63.1 178904	2	AL1354989		AL1354989	Homo sapi
c 2	24.6	63.1 184748	2	AL1160051		AL1160051	Homo sapi
c 3	24.2	62.1 67982	2	AC068869		AC068869	Homo sapi
c 4	24.2	62.1 107839	2	AP000574		AP000574	Homo sapi
c 5	24.2	62.1 114478	2	AP000489		AP000489	Homo sapi
c 6	24.2	62.1 123300	2	AP000406		AP000406	Homo sapi
c 7	24.2	62.1 128206	2	AP001258		AP001258	Homo sapi
c 8	24.2	62.1 225142	2	AP002358		AP002358	Homo sapi
c 9	24.2	62.1 226020	2	AC087589		AC087589	Homo sapi
c 10	24.6	61.5 195496	2	AL136014		AL136014	Homo sapi
c 11	24.6	61.5 203257	9	AC017377		AC017377	Homo sapi
c 12	23.8	61.0 1752	10	AF244362		AF244362	Mus muscu
c 13	23.2	59.5 49743	2	AC017211		AC017211	Drosophili
c 14	23.2	59.5 198721	2	AC010060		AC010060	Drosophili
c 15	23.5	59.5 274585	3	AE01533		AE01533	Drosophili
c 16	23.5	59.0 5767	10	DS3002		DS3002	Mouse mRNA
c 17	23.5	59.0 12485	1	AE004962		AE004962	Pseudomon
c 18	23.5	59.0 68790	9	HS287H17		HS287H17	Human DNA
c 19	23.5	59.0 36117	2	AC008700		AC008700	Homo sapi
c 20	23.5	59.0 182127	2	AP001842		AP001842	Homo sapi
c 21	23.5	59.0 184284	2	AC025582		AC025582	Mus muscu
c 22	23.5	59.0 192110	2	AP004070		AP004070	Orf2a sat
c 23	23.5	59.0 226899	2	AL159188		AL159188	Homo sapi
c 24	22.8	58.5 130192	9	AL157832		AL157832	Human DNA
c 25	22.8	58.5 157058	2	AL155725		AL155725	Homo sapi
c 26	22.8	58.5 187344	9	AL1354873		AL1354873	Human DNA
c 27	22.6	57.9 174253	2	AL025872		AL025872	Human NAD+
c 28	22.4	57.4 1148	9	MENAD1G5		MENAD1G5	M. fascicula
c 29	22.4	57.4 1285	9	HSU65268		HSU65268	Human clone
c 30	22.4	57.4 1343	9	BC001920		BC001920	Homo sapi
c 31	22.4	57.4 1362	9	BC000933		BC000933	Homo sapi
c 32	22.4	57.4 1370	9	HSRNAD1H		HSRNAD1H	H. sapiens m
c 33	22.4	57.4 1506	9	HSU40272		HSU40272	Human NAD+
c 34	22.4	57.4 18234	9	HS1DITRAP		HS1DITRAP	Zeb129 H. sapiens I
c 35	22.4	57.4 191923	9	AC087886		AC087886	Ac087886
c 36	22.4	57.4 230516	9	HSU52111		HSU52111	Human clone
c 37	22.2	55.9 31600	2	AC019859		AC019859	Drosophili
c 38	22.2	56.9 151162	9	AC003364		AC003364	Human Chr
c 39	22.2	56.9 156508	3	AC027581		AC027581	Drosophili
c 40	22.2	56.9 158648	2	AC021853		AC021853	Homo sapi
c 41	22.2	56.9 170089	3	AC007925		AC007925	Drosophili
c 42	22.2	56.9 188090	3	AC011625		AC011625	Homo sapi
c 43	22.2	56.9 306848	3	AE003464		AE003464	Drosophili
c 44	22.2	56.4 123386	8	FL2F1		FL2F1	Arabidops
c 45	22.2	56.4 134331	2	RN462P8		RN462P8	Rattus no

## ALIGNMENTS

RESULT 1  
AL334989/c  
LOCUS 178904 bp DNA DEFINITION Homo Sapiens chromosome 9 clone RP11-537H15, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 2 unordered pieces.  
ACCESSION AL334989  
VERSION AL334989.8 GI:15131225  
KEYWORDS HPGS\_PHASEL; HPGS\_ACTIVEFIN; HPGS\_DRAFT; HPGS\_FULLTOP.  
SOURCE Homo sapiens  
ORGANISM Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
REFERENCE Chapman,J.  
AUTHORS direct Submission  
TITLE C310 USA, UK. E-mail enquiries: hungquery@sanger.ac.uk  
JOURNAL requests: clonerequest@sanger.ac.uk  
On Aug 9, 2001 this sequence version replaced gi:14715324.  
COMMENT SUMMARIES  
----- Genome Center

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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COMMENT  
 Center: Sanger Centre  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: humquery@sanger.ac.uk  
 ----- Project Information  
 Center project name: BA53RH15  
 ----- Summary Statistics  
 Assembly program: XGAP4; version 4.5  
 Sequencing vector: plasmid; L08752; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Consensus quality: 177432 bases at least Q40  
 Consensus quality: 177660 bases at least Q30  
 Consensus quality: 177769 bases at least Q20  
 Insert size: 178804; sum-of-contigs  
 Insert size: 187738; 38.1% error; agarose-fp  
 Insert size: 16,40x in Q20 bases; sum-of-contigs Quality  
 coverage: 15.62x in Q20 bases; agarose-fp  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 2 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 176743: contig of 176743 bp in length  
 \* 1 176744 176843: gap of 100 bp  
 \* 176844 178904: contig of 2061 bp in length.  
 FEATURES  
 source  
 1. 178904  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="9"  
 /clone="RP1-53RH15"  
 /clone\_id="RPCI-11.2"  
 1. 176743  
 /note="assembly\_fragment:03560  
 fragment\_chain:1  
 clone\_end:T7  
 vector\_side:left"  
 misc\_feature  
 /note="assembly\_fragment:06048  
 fragment\_chain:1"  
 BASE COUNT 52784 a 40958 c 39193 g 45869 t 100 others  
 ORIGIN  
 Query Match 63.1%; Score 24.6; DB 2; Length 178904;  
 Best Local Similarity 76.9%; Pid. No. 26;  
 Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 OY 1 aggaatggccttggggccttggaaatggcttatt 39  
 ||||| ||||| ||||| ||| ||| ||||| ||||| |||||  
 Db 164878 AGGGAAAGCCTCTGGACATAGATATGCCCTCTGATT 164840  
 RESULT 2  
 AL160051/C  
 LOCUS AL160051 184748 bp DNA HTG 27-JUN-2001  
 DEFINITION Homo sapiens chromosome 9 clone RP1-499G9, \*\*\* SEQUENCING IN  
 PROGRESS \*\*\*, 18 unordered pieces.  
 ACCESSION AL160051  
 VERSION AL160051.15  
 KEYWORDS HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 184748)  
 AUTHORS Plumb, B.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,  
  
 COMMENT  
 Center: Sanger Centre  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: humquery@sanger.ac.uk  
 ----- Project Information  
 Center project name: BA499G9  
 ----- Summary Statistics  
 Assembly Program: XGAP4; version 4.5  
 Sequencing vector: plasmid; L08752; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Consensus quality: 179564 bases at least Q40  
 Consensus quality: 180655 bases at least Q30  
 Consensus quality: 181686 bases at least Q20  
 Insert size: 183048; sum-of-contigs  
 Insert size: 195118; 7.3% error; agarose-fp  
 Quality coverage: 9.04x in Q20 bases; agarose-fp  
 coverage: 9.76x in Q20 bases; agarose-fp  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 18 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 13081: contig of 13081 bp in length  
 \* 13082 13181: gap of 100 bp  
 \* 13182 16206: contig of 3115 bp in length  
 \* 16297 16396: gap of 100 bp  
 \* 16397 57604: contig of 41208 bp in length  
 \* 57605 57704: gap of 100 bp  
 \* 57704 79988: contig of 22284 bp in length  
 \* 79989 80088: gap of 100 bp  
 \* 80089 95798: contig of 13701 bp in length  
 \* 95790 95889: gap of 100 bp  
 \* 95890 104909: contig of 9020 bp in length  
 \* 104910 105009: gap of 100 bp  
 \* 10501 117002: contig of 11993 bp in length  
 \* 117103 130856: gap of 100 bp  
 \* 130859 130958: gap of 100 bp  
 \* 130959 140048: contig of 9990 bp in length  
 \* 140049 140148: gap of 100 bp  
 \* 140149 146391: contig of 6249 bp in length  
 \* 146398 146497: gap of 100 bp  
 \* 146498 148555: contig of 2062 bp in length  
 \* 148560 148659: gap of 100 bp  
 \* 148660 154236: contig of 5577 bp in length  
 \* 154237 153359: gap of 100 bp  
 \* 154337 156523: contig of 2187 bp in length  
 \* 156524 156623: gap of 100 bp  
 \* 156624 166567: contig of 9944 bp in length  
 \* 166568 166671: gap of 100 bp  
 \* 166668 173995: contig of 7278 bp in length  
 \* 173995 174095: gap of 100 bp  
 \* 174095 177011: contig of 2322 bp in length  
 \* 177018 177117: gap of 100 bp  
 \* 177118 181410: contig of 4293 bp in length  
 \* 181411 181510: gap of 100 bp  
 \* 181511 184748: contig of 3238 bp in length.  
 FEATURES  
 source  
 1. 184748  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="9"  
 /clone="RP1-499G9"  
 /clone\_id="RPCI-11.2"  
 misc\_feature  
 1. 13081



7859 7958: gap of 100 bp  
 7959 8603: contig of 645 bp in length  
 \* \* \* \* \* 8604 8703: gap of 100 bp  
 8704 9350: contig of 647 bp in length  
 \* \* \* \* \* 9351 9450: gap of 100 bp  
 \* \* \* \* \* 9451 10065: contig of 615 bp in length  
 \* \* \* \* \* 10065 10165: gap of 100 bp  
 \* \* \* \* \* 10166 10791: contig of 632 bp in length  
 \* \* \* \* \* 10798 10897: gap of 100 bp  
 \* \* \* \* \* 10898 11522: contig of 625 bp in length  
 \* \* \* \* \* 11523 11622: gap of 100 bp  
 \* \* \* \* \* 11623 12251: contig of 629 bp in length  
 \* \* \* \* \* 12252 12351: gap of 100 bp  
 \* \* \* \* \* 12352 12988: contig of 637 bp in length  
 \* \* \* \* \* 12989 13088: gap of 100 bp  
 \* \* \* \* \* 13089 13708: contig of 620 bp in length  
 \* \* \* \* \* 13709 13908: gap of 100 bp  
 \* \* \* \* \* 13809 14413: contig of 665 bp in length  
 \* \* \* \* \* 14454 14553: gap of 100 bp  
 \* \* \* \* \* 14554 15193: contig of 640 bp in length  
 \* \* \* \* \* 15194 15293: gap of 100 bp  
 \* \* \* \* \* 15294 15925: contig of 632 bp in length  
 \* \* \* \* \* 15926 16025: gap of 100 bp  
 \* \* \* \* \* 16026 16601: contig of 615 bp in length  
 \* \* \* \* \* 16641 16740: gap of 100 bp  
 \* \* \* \* \* 16741 17378: contig of 638 bp in length  
 \* \* \* \* \* 17379 17478: gap of 100 bp  
 \* \* \* \* \* 17479 18084: contig of 606 bp in length  
 \* \* \* \* \* 18085 18188: gap of 100 bp  
 \* \* \* \* \* 18185 18825: contig of 641 bp in length  
 \* \* \* \* \* 18826 18925: gap of 100 bp  
 \* \* \* \* \* 18926 19545: contig of 620 bp in length  
 \* \* \* \* \* 19546 19645: gap of 100 bp  
 \* \* \* \* \* 19646 20303: contig of 658 bp in length  
 \* \* \* \* \* 20304 20403: gap of 100 bp  
 \* \* \* \* \* 20404 21035: contig of 632 bp in length  
 \* \* \* \* \* 21036 21135: gap of 100 bp  
 \* \* \* \* \* 21136 21797: contig of 661 bp in length  
 \* \* \* \* \* 21797 21895: gap of 100 bp  
 \* \* \* \* \* 21897 22533: contig of 637 bp in length  
 \* \* \* \* \* 22534 22633: gap of 100 bp  
 \* \* \* \* \* 22634 23256: contig of 623 bp in length  
 \* \* \* \* \* 23257 23356: gap of 100 bp  
 \* \* \* \* \* 23357 24007: contig of 651 bp in length  
 \* \* \* \* \* 24008 24107: gap of 100 bp  
 \* \* \* \* \* 24108 24151: contig of 644 bp in length  
 \* \* \* \* \* 24152 24851: gap of 100 bp  
 \* \* \* \* \* 24852 25480: contig of 529 bp in length  
 \* \* \* \* \* 25481 25580: gap of 100 bp  
 \* \* \* \* \* 25581 26192: contig of 612 bp in length  
 \* \* \* \* \* 26193 26292: gap of 100 bp  
 \* \* \* \* \* 26293 26889: contig of 607 bp in length  
 \* \* \* \* \* 26900 26999: gap of 100 bp  
 \* \* \* \* \* 27000 27609: contig of 610 bp in length  
 \* \* \* \* \* 27610 27709: gap of 100 bp  
 \* \* \* \* \* 27710 28433: contig of 624 bp in length  
 \* \* \* \* \* 28434 28433: gap of 100 bp  
 \* \* \* \* \* 28434 29067: contig of 634 bp in length  
 \* \* \* \* \* 29068 29167: gap of 100 bp  
 \* \* \* \* \* 29168 29822: contig of 655 bp in length  
 \* \* \* \* \* 29823 29922: gap of 100 bp  
 \* \* \* \* \* 29923 30589: contig of 667 bp in length  
 \* \* \* \* \* 30590 30689: gap of 100 bp  
 \* \* \* \* \* 30690 31333: contig of 644 bp in length  
 \* \* \* \* \* 31334 31433: gap of 100 bp  
 \* \* \* \* \* 31434 32076: contig of 643 bp in length  
 \* \* \* \* \* 32077 32176: gap of 100 bp  
 \* \* \* \* \* 32177 32917: contig of 641 bp in length  
 \* \* \* \* \* 32818 32917: gap of 100 bp  
 \* \* \* \* \* 32918 33544: contig of 627 bp in length  
 \* \* \* \* \* 33545 33644: gap of 100 bp  
 \* \* \* \* \* 33645 34293: contig of 649 bp in length  
 \* \* \* \* \* 34294 34393: gap of 100 bp

Query Match 62.1%; Score 24.2; DB 2; Length 67982;  
 Best Local Similarity 78.4%; Pred. No. 37; Mismatches 0; Indels 0; Gaps 0;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aagagatggccttggggcccttggaaatggccctta 37  
 Locus AP000574/C  
 Definition Homo sapiens chromosome 11 clone CMB9-49B9 map 11q12, WORKING DRAFT  
 Sequence 9 unordered pieces.  
 Accession AP000574  
 Version AP000574.2  
 KeyWords HTGS\_PHASE1, HTGS\_DRAFT  
 Source Homo sapiens DNA, clone:CMB9-49B9.  
 Organism Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 Reference 1 (bases 1 to 107839)  
 Authors Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
 Fujiyama,A., Yada,T., Notoki,Y., Watanabe,H. and Sakaki,Y.  
 Title Homo sapiens 107,839 genomic DNA of 11q12  
 Reference Published Only in Database (1999) In press  
 Authors Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
 2 (bases 1 to 107839)



Assembly program: Phrap; version 0.990329  
 Consensus quality: 109628 bases at least 040  
 Consensus quality: 112052 bases at least 030  
 Consensus quality: 113108 bases at least 020  
 Insert size: 113878; sum-of-contigs  
 Quality coverage: 6.65x in 020 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 58724 contig of 58724 bp in length  
 58825 83984 contig of 25160 bp in length  
 83984 95379 contig of 11295 bp in length  
 95480 105075 contig of 6225 bp in length  
 105176 111400 contig of 1838 bp in length  
 111501 113338 contig of 1040 bp in length

Sequence updated (04-Nov-1999)

Sequence updated (26-May-2000)

\* NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

\* consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

\* 1 58724: contig of 58724 bp in length  
 \* 58725 58824: gap of 100 bp  
 \* 58925 83984: contig of 25160 bp in length  
 \* 83985 84084: gap of 100 bp  
 \* 84065 95379: contig of 11295 bp in length  
 \* 95380 95479: gap of 100 bp  
 \* 95480 105075: contig of 6225 bp in length  
 \* 105076 105175: gap of 100 bp  
 \* 105176 111400: contig of 1838 bp in length  
 \* 111401 111501: gap of 100 bp  
 \* 111501 113338: contig of 1040 bp in length  
 \* 113339 113438: gap of 100 bp  
 \* 113439 114478: contig of 1040 bp in length.

Location/Qualifiers

1. 114478

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="11"  
 /map="11q13"  
 /clone="CHB9-7F5"

misc\_feature

1. 58724

/note="assembly\_fragment"

misc\_feature

58825. .83984

/note="assembly\_fragment clone\_end:r7 vector\_side:left"

misc\_feature

84085. .95379

/note="assembly\_fragment"

misc\_feature

95480. .105075

/note="assembly\_fragment"

105176. .111400

/note="assembly\_fragment clone\_end:SP6 vector\_side:right"

misc\_feature

111501. .113338

/note="assembly\_fragment"

113439. .114478

/note="assembly\_fragment"

BASE COUNT

33314 a 23593 c 23225 g 33745 t 600 others

RESULT 6

AP000406/c

LOCUS AP000406 123300 bp DNA DEFINITION Homo sapiens chromosome 11 clone CMB9-21D9 map 11q12, WORKING DRAFT

SEQUENCE, 4 unordered pieces.

REFERENCE AP000406

VERSION AP000406.4 GI:992770

KEYWORDS Bmg; Bmg; PHASE; HTGS\_DRAFT.

SOURCE Homo sapiens DNA; clone:CMB9-21D9.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 123300)

AUTHORS Hattori,M., Ishii,K., Toyota,A., Taylor,T.D., Hong-Seq,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE 123,300 genomic DNA of 11q12

JOURNAL Published Only in Database (1999) In press

REFERENCE 2 (bases 1 to 123300)

AUTHORS Hattori,M., Ishii,K., Toyota,A., Taylor,T.D., Hong-Seq,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

COMMENT Tel:81-42-778-9231, Fax:81-42-778-9241.

On Aug 26, 2000 this sequence version replaced gi:8118745.

-----

Project Information

Center: RIKEN Genomic Sciences Center (GSC)

Center project name: HumanR1

Center clone name: CMB9-21D9

-----

Summary Statistics

Web site: <http://hgp.gsc.riken.go.jp/>

Contact: [hattori@gsc.riken.go.jp](mailto:hattori@gsc.riken.go.jp)

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Center: RIKEN Genomic Sciences Center (GSC)

Center project name: HumanR1

Center clone name: CMB9-21D9

-----

Sequencing vector: PCR products; 100% of reads

Chemistry: Dye-terminator

Assembly Program: Phrap; version 0.990329

Consensus quality: 121846 bases at least 040

Consensus quality: 122507 bases at least 030

Consensus quality: 122832 bases at least 020

Insert size: 123000; sum-of-contigs

Quality coverage: 13.07x in 020 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 61533 contig of 61533 bp in length  
 61534 106881 contig of 45248 bp in length  
 106982 112565 contig of 12584 bp in length  
 112566 123300 contig of 3635 bp in length.

\* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

\* 1 61533: contig of 61533 bp in length  
 \* 61534 61633: gap of 100 bp  
 \* 61634 106881: contig of 45248 bp in length  
 \* 106882 106981: gap of 100 bp

Insert size: 127906; sum-of-contigs  
 Quality coverage: 9.70x in Q20 bases; sum-of-contigs

-----

FEATURES  
 source  
 1. 119666  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="11"  
 /map="11q12"  
 /clone="CMB9-21D9"  
 1. 61533  
 /note="assembly\_fragment"  
 misc\_feature  
 61634 106881  
 /note="assembly\_fragment"  
 misc\_feature  
 106882 119565  
 /note="assembly\_fragment:clone\_end:SP6 vector\_side:right"  
 misc\_feature  
 119666 123300  
 /note="assembly\_fragment:clone\_end:T7 vector\_side:right"  
 BASE COUNT 36534 a 25670 c 26307 g 34489 t 300 others  
 ORIGIN

Query Match 62.1%; Score 24.2; DB 2; Length 123300;  
 Best Local Similarity 78.4%; Pred. No. 37;  
 Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

DEFINITION Homo sapiens chromosome 11 clone CMB9-103D1 map 11q12, WORKING  
 DRAFT SEQUENCE, 4 unordered pieces.

ACCESSION AP001258  
 VERSION AP001258\_3 GI:10716815  
 KEYWORDS HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE Homo sapiens DNA, clone:CMB9-103D1.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 128206)  
 AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE JOURNAL Submitted (23-FEB-2000) Masahira Hattori, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan  
 (E-mail:hattori@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/ ,  
 Tel:81-42-778-9923, Fax:81-42-778-9924)

COMMENT On oct 7, 2000 this sequence version replaced g1:8117651.  
 ----- Genome Center  
 Center: RIKEN Genomic Sciences Center(GSC)  
 Center code: RIKEN  
 Center web site: http://hgp.gsc.riken.go.jp/  
 Contact: hattori@gsc.riken.go.jp  
 ----- Project Information  
 Center project name: Humdraft11  
 Center clone name: CMB9-103D1  
 ----- Summary Statistics  
 Sequencing vector: PCR products; 100% of reads  
 Chemistry: Dye-terminator ET-Emersham; 100% of reads  
 Assembly program: Phrap; version 0.990229  
 Consensus quality: 12634 bases at least Q40  
 Consensus quality: 127174 bases at least Q30  
 Consensus quality: 127641 bases at least Q20

FEATURES  
 source  
 1. 89511  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="11"  
 /map="11q12"  
 /clone="CMB9-103D1"  
 1. 89512 89511: contig of 89511 bp in length  
 108014 119129: contig of 18302 bp in length  
 119230 128206: contig of 8977 bp in length.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 4 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will be  
 \* be preserved.  
 \* 1 89512 89511: contig of 89511 bp in length  
 \* 89612 107913: contig of 18302 bp in length  
 \* 107914 108013: gap of 100 bp  
 \* 108014 119129: contig of 11116 bp in length.  
 \* 119130 119229: gap of 100 bp  
 119230 128206: contig of 8977 bp in length.  
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 FEATURES  
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 1. 128206  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="11"  
 /map="11q12"  
 /clone="CMB9-103D1"  
 1. 89511  
 /note="assembly\_fragment:clone\_end:T7 vector\_side:left"  
 misc\_feature  
 89612 107913  
 /note="assembly\_fragment"  
 misc\_feature  
 108014 119129  
 /note="assembly\_fragment:clone\_end:SP6 vector\_side:left"  
 misc\_feature  
 119230 128206  
 /note="assembly\_fragment"  
 BASE COUNT 37466 a 26270 c 26422 g 37748 t 300 others  
 ORIGIN

Query Match 62.1%; Score 24.2; DB 2; Length 128206;  
 Best Local Similarity 78.4%; Pred. No. 37;  
 Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

DEFINITION Homo sapiens chromosome 11 clone RP11-1036E20 map 11q, WORKING  
 DRAFT SEQUENCE, 13 unordered pieces.

ACCESSION AP002358  
 VERSION AP002358\_2 GI:1225034  
 KEYWORDS HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE Homo sapiens DNA, clone:RP11-1036E20.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 225142)  
 AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE Homo sapiens 225,142 genomic DNA of 11q





Consensus quality: 194462 bases at least Q30  
 Consensus quality: 194143 bases at least Q20  
 Insert size: 195395; sum-of-contigs  
 Insert size: 179111; 5.8% error; agarose-fp  
 Quality coverage: 7.28x in Q20 bases; sum-of-contigs Quality coverage: 8.01x in Q20 bases; agarose-fp  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 2 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved  
 \* 1 103853: contig of 103853 bp in length  
 \* 103854 103953: gap of 100 bp  
 \* 103946: contig of 91543 bp in length.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /chromosome="10"  
 /clone="RP11-31B15N7"  
 /clone\_id="RPCI-11.2"  
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 fragment\_chain:1"  
 misc\_feature  
 misc\_feature  
 /note="assembly fragment:03176  
 fragment\_chain:1"  
 misc\_feature  
 misc\_feature  
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 ORIGIN

Query Match  
 Best Local Similarity 61.5%; Score 24; DB 2; Length 195496;  
 Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 Qy 6 atggccttggggccctggaaatggcttccta 37  
 Qy 6 atggccttggggccctggaaatggcttccta 37  
 Qy 6 atggccttggggccctggaaatggcttccta 37  
 Db 144662 ATTCCTTGGCCTTGGATTTCGCCTTA 144631

RESULT 12  
 AF244362/c  
 LOCUS AF244362 mRNA  
 DEFINITION Mus musculus ubiquitin-protein ligase UBE3B (Ube3b) mRNA, partial  
 ACCSSION AF244362  
 VERSION AF244362.1 GI:10436098  
 KEYWORDS  
 SOURCE  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE  
 1 (bases 1 to 1752)  
 AUTHORS Lomaxab, M.I., Huang, L., Choab, Y., Gonda, T.L. and Altschulerab, R.A.  
 TITLE Differential display and gene arrays to examine auditory plasticity  
 JOURNAL Hear. Res. 147 (1-2), 293-302 (2000)  
 MEDLINE 2042030  
 REFERENCE  
 AUTHORS Lomax, M.I. and Huang, L.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-MAR-2000) Dept. of Otolaryngology, Kresge Hearing Research Institute, 1150 W. Med. Ctr. Dr., Ann Arbor, MI 48109, USA  
 FEATURES  
 source  
 /organism="Mus musculus"  
 /strain="C57BL6/J"  
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 /clone="IMAGE:552315"  
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 /gene="Ube3b"  
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 /ab\_xref="GI: 10436099"  
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 SPSRPLIGEATLPPKPSIRQEVSDQDFTLGSVLRGFFTIRKREPGGRPLTS  
 CFNLKIKPNNYSKVKRERKLAISNAGFELS"  
 REFERENCE  
 AUTHORS Smith, D.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-NOV-1999) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA  
 REFERENCE  
 AUTHORS Smith, D.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-MAY-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA  
 REFERENCE  
 AUTHORS Smith, D.R.  
 TITLE Direct Submission

JOURNAL Submitted (15-JUN-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA  
 REFERENCE 5 (bases 1 to 203257)  
 AUTHORS Smith, D.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-JUN-2001) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA  
 COMMENT On May 7, 2000 this sequence version replaced gi:6539205.  
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 source  
 1. 103946  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="10"  
 /clone="RP11-31B15N7"  
 /clone\_id="RPCI-11.2"  
 1. 103853  
 /note="assembly fragment:03932  
 fragment\_chain:1"  
 misc\_feature  
 misc\_feature  
 BASE COUNT 68225 a 36293 c 35286 g 63453 t  
 ORIGIN

Query Match  
 Best Local Similarity 61.5%; Score 24; DB 9; Length 203257;  
 Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 Qy 6 atggccttggggccctggaaatggcttccta 37  
 Db 144662 ATTCCTTGGCCTTGGATTTCGCCTTA 144631

RESULT 12  
 AF244362/c  
 LOCUS AF244362 mRNA  
 DEFINITION Mus musculus ubiquitin-protein ligase UBE3B (Ube3b) mRNA, partial  
 ACCSSION AF244362  
 VERSION AF244362.1 GI:10436098  
 KEYWORDS  
 SOURCE  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE  
 1 (bases 1 to 1752)  
 AUTHORS Lomaxab, M.I., Huang, L., Choab, Y., Gonda, T.L. and Altschulerab, R.A.  
 TITLE Differential display and gene arrays to examine auditory plasticity  
 JOURNAL Hear. Res. 147 (1-2), 293-302 (2000)  
 MEDLINE 2042030  
 REFERENCE  
 AUTHORS Lomax, M.I. and Huang, L.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-MAR-2000) Dept. of Otolaryngology, Kresge Hearing Research Institute, 1150 W. Med. Ctr. Dr., Ann Arbor, MI 48109, USA  
 FEATURES  
 source  
 /organism="Mus musculus"  
 /strain="C57BL6/J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:552315"  
 /dev\_stage="embryo"  
 /gene="Ube3b"  
 <1..1752  
 /gene="Ube3b"  
 /gene="Ube3b"  
 /codon\_start=2  
 /product="ubiquitin-protein ligase UBE3B"  
 /protein\_id="AA316783.1"  
 /ab\_xref="GI: 10436099"  
 /translation="KISIHIIMAHFRMHTQKNTAALISGFRSLIKPEWIRMSTE  
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 SPSRPLIGEATLPPKPSIRQEVSDQDFTLGSVLRGFFTIRKREPGGRPLTS  
 CFNLKIKPNNYSKVKRERKLAISNAGFELS"  
 REFERENCE  
 AUTHORS Smith, D.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-MAY-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02453, USA  
 REFERENCE  
 AUTHORS Smith, D.R.  
 TITLE Direct Submission







Query Match 99.5%; Score 23.2;  
Best Local Similarity 89.3%; Pred. No.  
Matches 25; Conservative 0; Mismatch 0;  
Qy 8 ggcttggggcttggaaatggctct 35  
||||||| ||||| ||||| ||||| |||||  
.Db 138449 GGCTTGGGGACGGCATGGCCCT 138422

Search completed: January 29, 2002, 21:25:11  
-Job time: 1819 sec

Query Match 99.5%; Score 23.2;  
Best Local Similarity 89.3%; Pred. No.  
Matches 25; Conservative 0; Mismatch 0;  
Qy 8 ggcttggggcttggaaatggctct 35  
||||||| ||||| ||||| ||||| |||||  
.Db 138449 GGCTTGGGGACGGCATGGCCCT 138422

Search completed: January 29, 2002, 21:25:11  
-Job time: 1819 sec